Sub A1

SEQUENCE PROTOCOL

<110> Degussa-Hüls AG

<120> New nucleotide sequences coding for the ptsH gene

<130> 990219 BT

<140>
<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1
<211> 480
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (163)..(429)
<223> ptsH wild-type gene

<400> 1

```
ggacattgtt tttgcttccg gtaacgtggc aaaacgaaca atgtctcact agactaaagt 60

gagatcgaca ttaaatcccc tcccttgggg ggtttaacta acaaatcgct gcgccctaat 120

ccgttcggat taacggcgta gcaacacgaa aggacacttt cc atg gct tcc aag    174
                                              Met Ala Ser Lys
                                                1

act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc   222
Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
  5                  10                  15                  20

atc atc gct gaa gcg gct gct gag tac gac gac gaa atc ttg ctg acc   270
Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr
                 25                  30                  35

ctg gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc   318
Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu
             40                  45                  50

atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc   366
Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr
         55                  60                  65

tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag   414
Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
     70                  75                  80

gac ctt gac gct gag taaacaacgc tctgcttgtt aaaagctcgt tagaagcttg   469
Asp Leu Asp Ala Glu
 85

ttaaaagcgg t                                                     480
```

<210> 2
<211> 89

Sub A1

<212> PRT
<213> Corynebacterium glutamicum

<400> 2

```
Met Ala Ser Lys Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala
 1               5                  10                  15

Arg Pro Ala Ser Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu
            20                  25                  30

Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
        35                  40                  45

Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
    50                  55                  60

Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
65                  70                  75                  80

Leu Ile Ala Gln Asp Leu Asp Ala Glu
                85
```

<210> 3
<211> 480
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (163)..(429)
<223> ptsH allele

<400> 3

```
ggacattgtt tttgcttccg gtaacgtggc aaaacgaaca atgtctcact agactaaagt 60

gagatcgaca ttaaatcccc tcccttgggg ggtttaacta acaaatcgct gcgccctaat 120

ccgttcggat taacggcgta gcaacacgaa aggacacttt cc atg gct tcc aag    174
                                                Met Ala Ser Lys
                                                  1

act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc    222
Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
  5                  10                  15                  20

atc atc gct gaa acg gct gct gag tac gac gac gaa atc ttg ctg acc    270
Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr
                25                  30                  35

ctg gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc    318
Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu
            40                  45                  50

atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc    366
Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr
        55                  60                  65

tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag    414
Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
    70                  75                  80

gac ctt gac gct gag taaacaacgc tctgcttgtt aaaagctcgt tagaagcttg    469
```

Sub A1

Asp Leu Asp Ala Glu
85

ttaaaagcgg t 480

<210> 4
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 4

Met Ala Ser Lys Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala
1 5 10 15

Arg Pro Ala Ser Ile Ile Ala Glu Thr Ala Ala Glu Tyr Asp Asp Glu
20 25 30

Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
35 40 45

Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
50 55 60

Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
65 70 75 80

Leu Ile Ala Gln Asp Leu Asp Ala Glu
85

<210> 5
<211> 20
<212> DNA
<213> Corynebacterium glutamicum

<220>
<223> Primer ptsHexp1

<400> 5
accactggtg caatctccat 20

<210> 6
<211> 20
<212> DNA
<213> Corynebacterium glutamicum

<220>
<223> Primer ptsHexp2

<400> 6
tttactcagc gtcaaggtcc 20